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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=7; day=16; hr=13; min=14; sec=47; ms=224;]

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Reviewer Comments:

1.

W402	Undefined organism found in <213> in SEQ ID (33)
W402	Undefined organism found in <213> in SEQ ID (34)
W402	Undefined organism found in <213> in SEQ ID (35)
W402	Undefined organism found in <213> in SEQ ID (36)
W402	Undefined organism found in <213> in SEQ ID (37)
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W402	Undefined organism found in <213> in SEQ ID (41)
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<210> 33
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For SEQ ID # 33 through 44, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown" or "Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank and, <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is

made in the laboratory, please indicate that the sequence is synthesized. Please make all necessary changes.

2.

W213	Artificial or Unknown found in <213> in SEQ ID (45)
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W213	Artificial or Unknown found in <213> in SEQ ID (53)
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W213	Artificial or Unknown found in <213> in SEQ ID (61)
W213	Artificial or Unknown found in <213> in SEQ ID (62)
W213	Artificial or Unknown found in <213> in SEQ ID (63)
W213	Artificial or Unknown found in <213> in SEQ ID (64) This error has occurred more than 20 times, will not be displayed

The warnings shown above are ok and require no response.

Application No: 10577003 Version No: 2.0

Input Set:

Output Set:

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Finished: 2009-06-23 16:31:49.350
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 379 ms
Total Warnings: 38
Total Errors: 0
No. of SeqIDs Defined: 72
Actual SeqID Count: 72

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (50)
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W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
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Input Set:

Output Set:

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Finished: 2009-06-23 16:31:49.350
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 379 ms
Total Warnings: 38
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No. of SeqIDs Defined: 72
Actual SeqID Count: 72

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	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Kharbanda, Surrender
Kufe, Donald

<120> Modulation of Interaction of MUC1 with MUC1 Ligands

<130> GENU:005US

<140> 10577003

<141> 2006-12-13

<150> PCT/US2004/034680

<151> 2004-10-21

<150> 60/514,198

<151> 2003-10-24

<150> 60/519,822

<151> 2003-11-12

<160> 72

<170> PatentIn version 3.3

<210> 1

<211> 164

<212> PRT

<213> Homo sapiens

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20 25 30

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35 40 45

Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Phe Asn
50 55 60

Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg
65 70 75 80

Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu
85 90 95

Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu
100 105 110

Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met Glu Thr
115 120 125

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
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20

25

30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
 50 55 60

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
 65 70 75 80

Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
 85 90 95

Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile
 100 105 110

Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
 115 120 125

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val
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<212> DNA

<213> Homo sapiens

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cagagaagtt cagtgccacg ctctactgag aagaatgctt ttaattcttc tctggaagat 180

cccagcaccg actactacca agagctgcag agagacattt ctgaaatggt ttgacagatt 240

tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 300

gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacat ggagacacag 360

ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 420

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<213> Homo sapiens

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Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser
50 55 60

Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
65 70 75 80

Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
85 90 95

Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
100 105 110

Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
115 120 125

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
130 135 140

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
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<213> Homo sapiens

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cagagaagtt cagtgccag ctctactgag aagaatgctc tgtctactgg ggtctctttc      180
tttttctgt cttttcacat ttcaaacctc cagtttaatt cctctctgga agatcccagc      240
accgactact accaagagct gcagagagac atttctgaaa tgtttttgca gatttataaa      300
caaggggggt ttctgggcct ctccaatatt aagttcaggc caggatctgt ggtggtacaa      360
ttgactctgg ccttccgaga aggtaccatc aatgtccacg acatggagac acagttcaat      420
cagtataaaa cggaagcagc ctctcgatat aacctgacga tctcagacgt cagcgtgagt      480
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<212> PRT
<213> Homo sapiens

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Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Thr
          35              40              45

Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln
          50              55              60

Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg
65              70              75              80

Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr
          85              90              95

Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu
          100              105              110

Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp
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Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
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<210> 8
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<212> DNA
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cagagaagtt cagtgccag caccgactac taccaagagc tgcagagaga cttttctgaa 180
atgtttttgc agatttataa acaagggggg tttctgggcc tctccaatat taagttcagg 240
ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 300
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 360
atctcagacg tcagcgtgag tgatgtgcca tttcctttct ctgcccagtc tggggctggg 420

<210> 9
<211> 130
<212> PRT
<213> Homo sapiens

<400> 9

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20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg
50 55 60

Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu
65 70 75 80

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
85 90 95

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
100 105 110

Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
115 120 125

Ala Gly
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<210> 10
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<213> Homo sapiens

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cagagaagtt cagtgccag ctctactgag aagaatgcta tccagcacc gactactacc 180
aagagctgca gagagacatt tctgaaatgg ccaggatctg tgggtgtaca attgactctg 240
gccttccgag aaggtaccat caatgtccac gacatggaga cacagttcaa tcagtataaa 300
acggaagcag cctctcgata taacctgacg atctcagacg tcagcgtgag tgatgtgcca 360
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<212> PRT
<213> Homo sapiens

<400> 11

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Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly
20 25 30

Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val
35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
85 90 95

Ala Gln Ser Gly Ala Gly
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<210> 12
<211> 306
<212> DNA
<213> Homo sapiens

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gtccacgaca tggagacaca gttcaatcag tataaaacgg aagcagcctc tcgatataac 240
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<212> PRT
<213> Homo sapiens

<400> 13

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65 70 75 80

Ala	Pro	Ala	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Ala	Ala	Thr	Trp	Gly	Gln	85	90	95
Asp	Val	Thr	Ser	Val	Pro	Val	Thr	Arg	Pro	Ala	Leu	Gly	Ser	Thr	Thr	100	105	110
Pro	Pro	Ala	His	Asp	Val	Thr	Ser	Ala	Pro	Asp	Asn	Lys	Pro	Ala	Pro	115	120	125
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	130	135	140
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	145	150	155
Ala	Pro	Asp	Asn	Arg	Pro	Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	His	165	170	175
Asn	Val	Thr	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	180	185	190
Val	His	Asn	Gly	Thr	Ser	Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	195	200	205
Ser	Thr	Pro	Phe	Ser	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	210	215	220
Leu	Ala	Ser	His	Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	225	230	235
Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	245	250	255
Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	260	265	270
Gln	Phe	Asn	Ser	Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	275	280	285
Leu	Gln	Arg	Asp	Ile	Ser	Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	290	295	300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
 305 310 315 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
 325 330 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
 340 345 350

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
 355 360 365

Ser Ala Gln Ser Gly Ala Gly
 370 375

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 cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180
 ctctccagcc acagcccggg ttcaggctcc tccaccactc agggacagga tgctactctg 240
 gccccggcca cggaaccagc ttcagggtca gctgccacct ggggacagga tgtcacctcg 300
 gtcccagtc cagggccagc cctgggctcc accacccgc cagcccacga tgtcacctca 360
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 actcctacca cccttgccag ccatagcacc aagactgatg ccagtagcac tcaccatagc 720
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<400> 15

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 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala